

Resource Summary Report

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MSAProbs

RRID:SCR_012982

Type: Tool

Proper Citation

MSAProbs (RRID:SCR_012982)

Resource Information

URL: <http://sourceforge.net/projects/msaprobs/>

Proper Citation: MSAProbs (RRID:SCR_012982)

Description: An open-source protein multiple sequence alignment algorithm, achieving the statistically highest alignment accuracy on popular benchmarks.

Abbreviations: MSAProbs

Synonyms: MSAProbs: Multiple Sequence Alignment

Resource Type: software resource

Defining Citation: [PMID:20576627](#)

Keywords: c++

Availability: GNU General Public License, v3

Resource Name: MSAProbs

Resource ID: SCR_012982

Alternate IDs: OMICS_00980

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260905T132730+0000

Ratings and Alerts

No rating or validation information has been found for MSAProbs.

No alerts have been found for MSAProbs.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Russ JE, et al. (2025) Competition between Der1 and ERAD-M substrates controls Hrd1 complex function. *Proceedings of the National Academy of Sciences of the United States of America*, 122(49), e2513595122.

Mendes LFS, et al. (2022) Resurrecting Golgi proteins to grasp Golgi ribbon formation and self-association under stress. *International journal of biological macromolecules*, 194, 264.

Matsutani M, et al. (2021) Comparative Genomics of Closely Related *Tetragenococcus halophilus* Strains Elucidate the Diversity and Microevolution of CRISPR Elements. *Frontiers in microbiology*, 12, 687985.

Jia H, et al. (2021) Direct Molecular Evidence for an Ancient, Conserved Developmental Toolkit Controlling Posttranscriptional Gene Regulation in Land Plants. *Molecular biology and evolution*, 38(11), 4765.

Ravarani CNJ, et al. (2020) Molecular determinants underlying functional innovations of TBP and their impact on transcription initiation. *Nature communications*, 11(1), 2384.

Garcia AK, et al. (2020) Reconstructing the evolutionary history of nitrogenases: Evidence for ancestral molybdenum-cofactor utilization. *Geobiology*, 18(3), 394.

Daugavet MA, et al. (2019) Features of a novel protein, rusticalin, from the ascidian *Styela rustica* reveal ancestral horizontal gene transfer event. *Mobile DNA*, 10, 4.

Zhan Q, et al. (2019) ProbPFP: a multiple sequence alignment algorithm combining hidden Markov model optimized by particle swarm optimization with partition function. *BMC bioinformatics*, 20(Suppl 18), 573.

Sng NJ, et al. (2019) A member of the CONSTANS-Like protein family is a putative regulator of reactive oxygen species homeostasis and spaceflight physiological adaptation. *AoB PLANTS*, 11(1), ply075.

Catchpole RJ, et al. (2019) The Evolution of Reverse Gyrase Suggests a Nonhyperthermophilic Last Universal Common Ancestor. *Molecular biology and evolution*, 36(12), 2737.

Garrido-Bigotes A, et al. (2019) Evolutionary Analysis of JAZ Proteins in Plants: An Approach in Search of the Ancestral Sequence. *International journal of molecular sciences*, 20(20).

Liu Q, et al. (2018) Ancient mechanisms for the evolution of the bicoid homeodomain's function in fly development. *eLife*, 7.

Catchpole R, et al. (2018) A series of new *E. coli*-*Thermococcus* shuttle vectors compatible with previously existing vectors. *Extremophiles : life under extreme conditions*, 22(4), 591.

Liu X, et al. (2018) In-depth comparative analysis of malaria parasite genomes reveals protein-coding genes linked to human disease in *Plasmodium falciparum* genome. *BMC genomics*, 19(1), 312.

Gu??rin F, et al. (2017) Flow cytometry sorting of nuclei enables the first global characterization of *Paramecium* germline DNA and transposable elements. *BMC genomics*, 18(1), 327.

Rodriguez JD, et al. (2017) Identification of a vacuolar proton channel that triggers the bioluminescent flash in dinoflagellates. *PloS one*, 12(2), e0171594.

Sechler AJ, et al. (2017) Whole genome sequence of two *Rathayibacter toxicus* strains reveals a tunicamycin biosynthetic cluster similar to *Streptomyces chartreusis*. *PloS one*, 12(8), e0183005.

Dias R, et al. (2017) Convergence of Domain Architecture, Structure, and Ligand Affinity in Animal and Plant RNA-Binding Proteins. *Molecular biology and evolution*, 34(6), 1429.

Kunz S, et al. (2017) The single cyclic nucleotide-specific phosphodiesterase of the intestinal parasite *Giardia lamblia* represents a potential drug target. *PLoS neglected tropical diseases*, 11(9), e0005891.

Li J, et al. (2015) A large-scale conformation sampling and evaluation server for protein tertiary structure prediction and its assessment in CASP11. *BMC bioinformatics*, 16, 337.